

Binding of the *Helicobacter pylori* OipA causes apoptosis of host cells via modulation of Bax/Bcl-2 levels

Omid Teymournejad¹, Ashraf Mohabati Mobarez^{1*}, Zuhair Mohammad Hassan², Amin Talebi Bezminabadi¹

¹Department of Bacteriology, Faculty of Medical Sciences, Tarbiat Modares University, Tehran, Iran.

²Department of Immunology, Faculty of Medical Sciences, Tarbiat Modares University, Tehran, Iran.

***Author for correspondence:** Ashraf Mohabati Mobarez, Department of Bacteriology, Faculty of Medical Sciences, Tarbiat Modares University, Tehran/ Iran. Email: mmmobarez@modares.ac.ir , Tell and Fax: (+98 21) 82883862

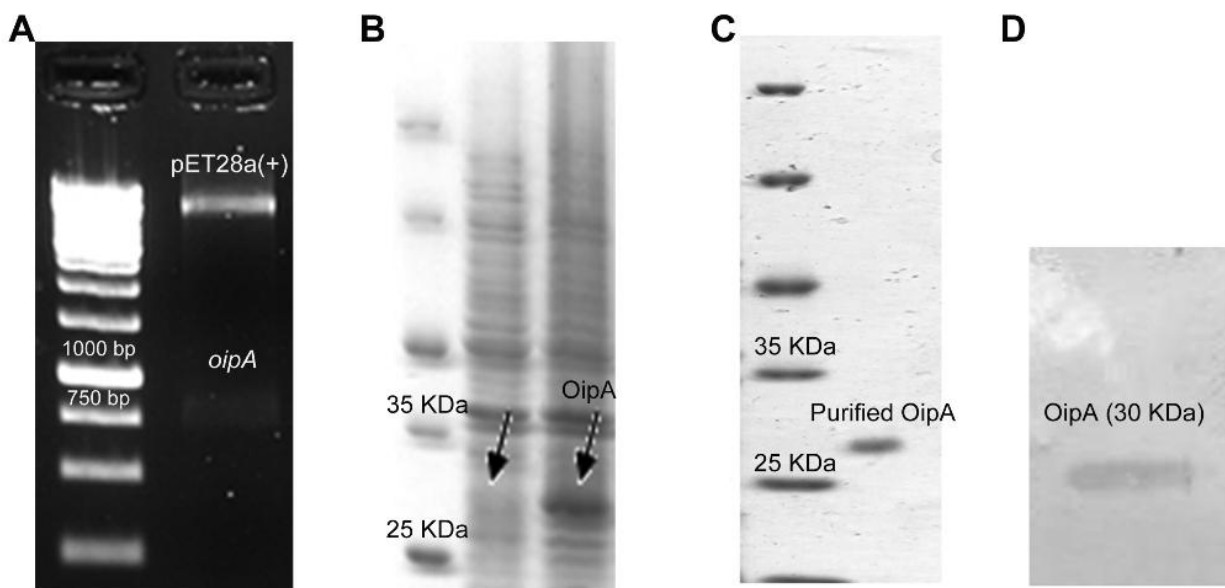
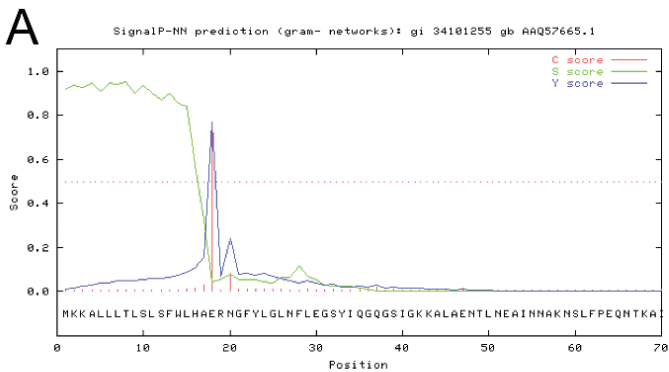
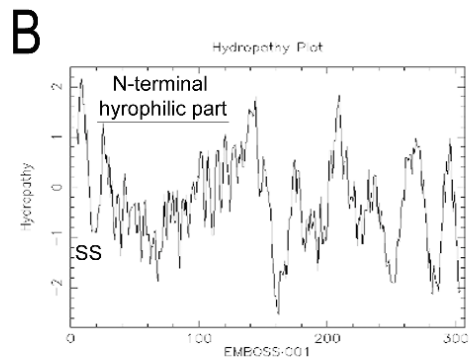


Fig. S1: Cloning, expression and purification of OipA.

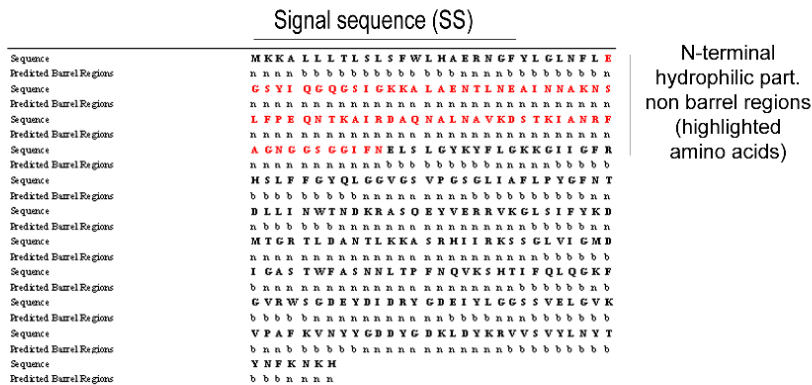
Cloning of OipA confirmed with double digestion by *NcoI* and *XhoI* restriction enzymes (A). Coomassie blue stained 12.5% SDS-PAGE gel showing induction and purification of the expressed OipA protein (B and C). Western blot analysis using the OipA antibody showed a single 30-kDa protein on nitrocellulose paper (D).



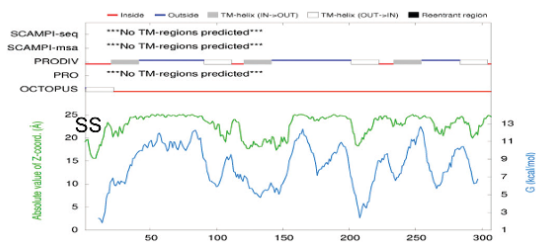
signal sequence (SS)



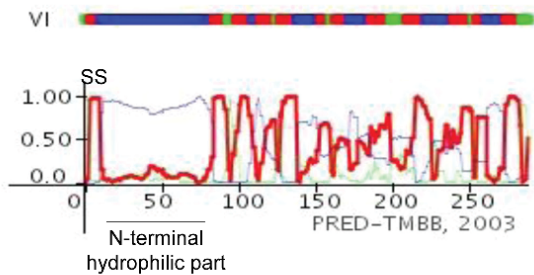
C



D

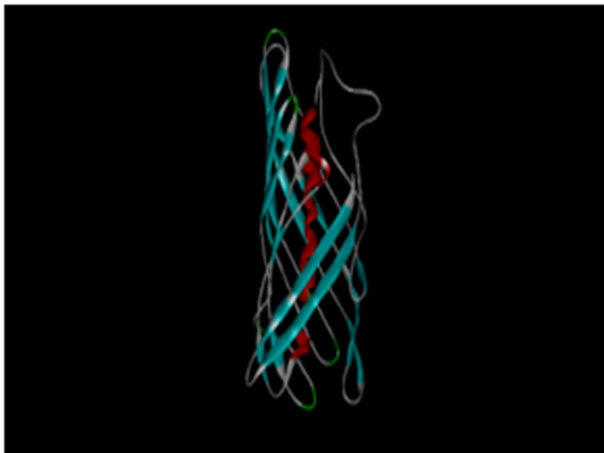


E



F

N-terminal hydrophilic part



G

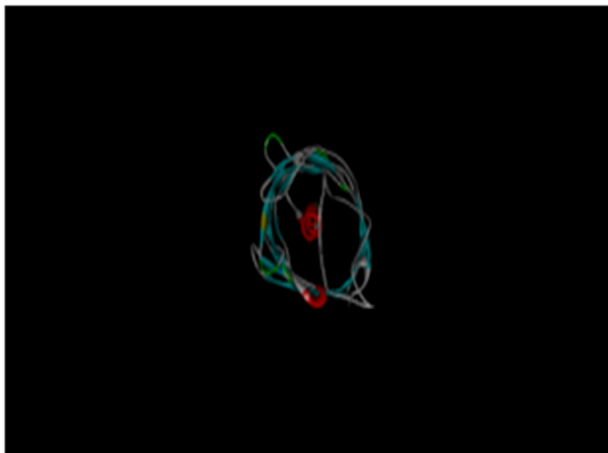


Fig. S2: *in-silico* prediction study on OipA showed that OipA is an auto-transporter.

Prediction of signal sequence of OipA using SignalP3.0 server (A). Hydropathy plot of OipA by EMBOSS Pepwindow server (B). Prediction of beta barrel of OipA in *H. pylori* outer membrane by TBBpred server; "n" refers to residues in non-barrel regions and "b" refers to residues in barrel region (C). Prediction of external and internal loops sequence of OipA by PRODIV-TMHMM server (D). Prediction of external and internal loops sequence of OipA by TMRPres2D server (E). Tertiary structure prediction of OipA by CPH model server (a protein homology server) and visualization with Discovery Studio Visualizer (F, G). The pattern recognition is according to profile-profile alignment guided by secondary structure and exposure predictions. The server has deleted approximately 30 hydrophilic amino acids from N-terminal sequence for finding the best match. Thus, the structures depicted in (F) and (G) are truncated forms of OipA and there must be thirty amino acid outside of the pore in N-terminal part.

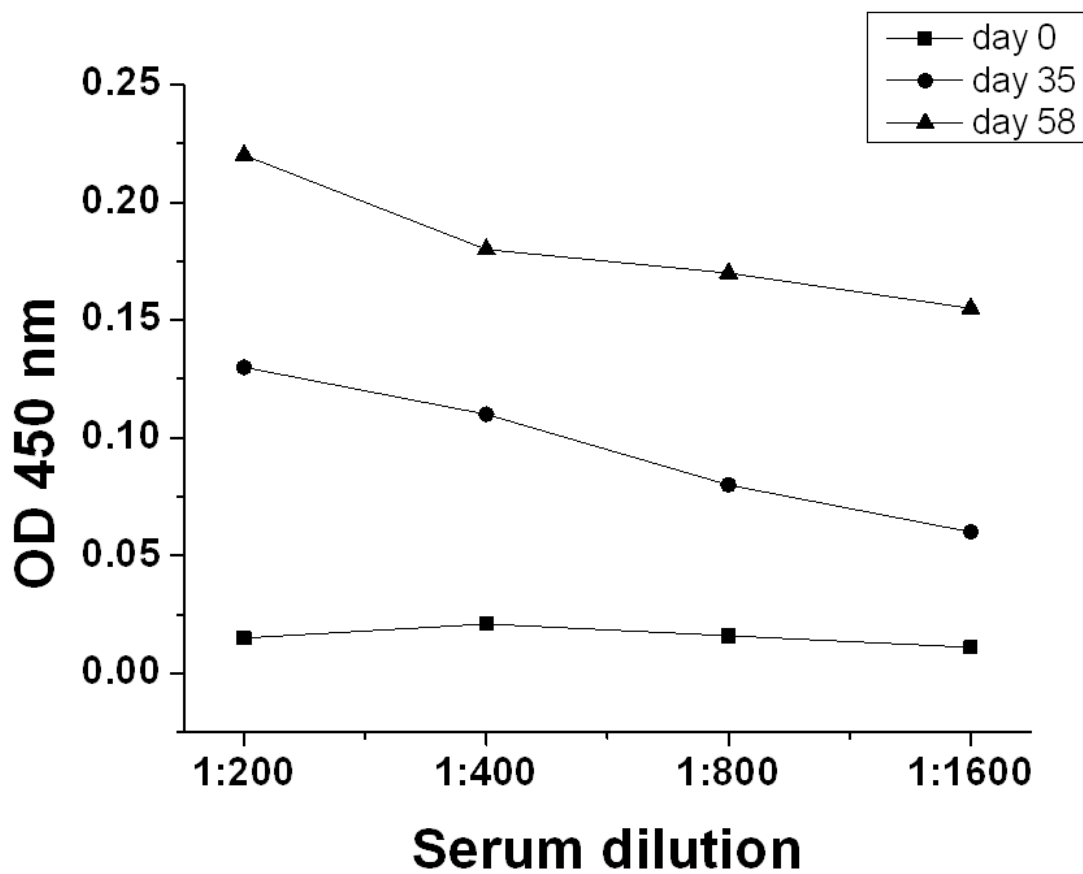


Fig. S3: Kinetic assessment of polyclonal antibody production against OipA.

A white female New Zealand rabbit was immunized 4 times with OipA with complete or incomplete frond adjuvant. The reactivity of diluted sera (serial dilutions from 1:200 to 1:1600) from the rabbit was measured at different time intervals by ELISA